

WHAT WE CLAIM IS:

1. A hybridization assay probe comprising an oligonucleotide which hybridizes to a target sequence present in nucleic acid derived from a *Cryptosporidium parvum* organism in a test sample under stringent conditions to form a probe:target hybrid stable for detection, said oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in the target sequence, wherein the target sequence is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19 and SEQ ID NO:20, and wherein said probe does not hybridize to nucleic acid derived from a *Cryptosporidium muris*, *Cryptosporidium baileyi* or *Crptosporidium wrairi* organism in the test sample to form a probe:non-target hybrid stable for detection under the stringent conditions.

2. The probe of claim 1, wherein the target sequence is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17.

3. The probe of claim 1, wherein the target sequence is selected from the group consisting of SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18.

4. The probe of claim 1, wherein the target sequence is selected from the group consisting of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 and SEQ ID NO:19.

5. The probe of claim 1, wherein the target sequence is selected from the group consisting of SEQ ID NO:8, SEQ ID NO:12, SEQ ID NO:16 and SEQ ID NO:20.

6. The probe of claim 1, wherein said oligonucleotide has an at least 10 contiguous base region which is at least 90% complementary to an at least 10 contiguous base region present in the target sequence.

7. The probe of claim 1, wherein said oligonucleotide has an at least 10 contiguous base region which is 100% complementary to an at least 10 contiguous base region present in the target sequence.

5 8. The probe of claim 1, wherein said probe is up to 100 bases in length.

9. The probe of claim 1, wherein said probe is from 12 to 50 bases in length.

10 10. The probe of claim 1, wherein said probe is from 18 to 35 bases in length.

11. The probe of claim 1, wherein said probe contains base sequences which hybridize to each other when not hybridized to the target sequence under the stringent conditions.  
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12. The probe of claim 1, wherein said probe comprises one or more base sequences which do not stably hybridize to nucleic acid derived from a *Cryptosporidium parvum* organism, or to nucleic acid derived from a non-target organism present in the test sample, under the stringent conditions.  
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13. The probe of claim 12, wherein said probe comprises two of said one or more base sequences, wherein said two base sequences hybridize to each other when said probe is not hybridized to the target sequence under the stringent conditions.  
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14. The probe of claim 1 further comprising a detectable label.

15. The probe of claim 1 further comprising a group of interacting labels.

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16. The probe of claim 15, wherein said interacting labels include a luminescent label and a quencher label.

5 17. The probe of claim 1, wherein said oligonucleotide includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety.

18. The probe of claim 1, wherein a pseudo peptide backbone joins at least a portion of the bases of said oligonucleotide.

10 19. The probe of claim 1, wherein the stringent conditions comprise 50 mM succinic acid, 1% (w/v) LLS, 7.5 mM aldrithiol-2, 0.6 M LiCl, 115 mM LiOH, 10 mM EDTA, 10 mM EGTA, 1.5% (v/v) ethyl alcohol (absolute), pH to 4.7, and a test sample temperature of about 60°C.

15 20. A hybridization assay probe comprising an oligonucleotide which hybridizes to a target sequence present in nucleic acid derived from a *Cryptosporidium parvum* organism in a test sample under stringent conditions to form a probe:target hybrid stable for detection, wherein the base sequence of said oligonucleotide is at least 80% complementary to the base sequence of the target sequence, wherein the target sequence has a base sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19 and SEQ ID NO:20, and wherein said probe does not hybridize to nucleic acid  
20 derived from a *Cryptosporidium muris*, *Cryptosporidium baileyi* or *Crptosporidium wrairi* organism in the test sample to form a probe:non-target hybrid stable for detection under the stringent conditions.

25 21. An oligonucleotide probe which hybridizes to a target sequence present in nucleic acid derived from a *Cryptosporidium parvum* organism in a test sample  
30 under stringent conditions to form a probe:target hybrid stable for detection, wherein the base

sequence of said probe is at least 80% complementary to the base sequence of the target sequence, wherein the target sequence is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19 and SEQ ID NO:20, and wherein said probe does not hybridize to nucleic acid derived from a *Cryptosporidium muris*, *Cryptosporidium baileyi* or *Crptosporidium wrairi* organism in the test sample to form a probe:non-target hybrid stable for detection under the stringent conditions.

22. An oligonucleotide probe which hybridizes to a target sequence present in nucleic acid derived from a *Cryptosporidium parvum* organism in a test sample under stringent conditions to form a probe:target hybrid stable for detection, wherein the base sequence of said probe is fully complementary to the base sequence of the target sequence, wherein the target sequence is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19 and SEQ ID NO:20, and wherein said probe does not hybridize to nucleic acid derived from a *Cryptosporidium muris*, *Cryptosporidium baileyi* or *Crptosporidium wrairi* organism in the test sample to form a probe:non-target hybrid stable for detection under the stringent conditions.

23. A probe mix comprising the probe of claim 1 and one or more helper oligonucleotides, each said helper oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence selected from the group consisting of SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43 and SEQ ID NO:44.

24. The probe mix of claim 23, wherein:

the target sequence of said probe is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:17 and SEQ ID NO:18; and

5 the target sequence of one of said helper oligonucleotides is selected from the group consisting of SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37 and SEQ ID NO:41.

25. The probe mix of claim 23, wherein:

10 the target sequence of said probe is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:17 and SEQ ID NO:18; and

the target sequence of one of said helper oligonucleotides is selected from the group consisting of SEQ ID NO:30, SEQ ID NO:34, SEQ ID NO:38 and SEQ ID NO:42.

15 26. The probe mix of claim 23, wherein:

the target sequence of said probe is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:17 and SEQ ID NO:18; and

20 the target sequence of one of said helper oligonucleotides is selected from the group consisting of SEQ ID NO:31, SEQ ID NO:35, SEQ ID NO:39 and SEQ ID NO:43.

27. The probe mix of claim 23, wherein:

25 the target sequence of said probe is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:17 and SEQ ID NO:18; and

the target sequence of one of said helper oligonucleotides is selected from the group consisting of SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40 and SEQ ID NO:44.

28. The probe mix of claim 23, wherein:

the target sequence of said probe is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:17 and SEQ ID NO:18; and

said one or more helper oligonucleotides include first and second helper oligonucleotides, wherein the target sequence of said first helper oligonucleotide is selected from the group consisting of SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37 and SEQ ID NO:41, and wherein the target sequence of said second helper oligonucleotide is selected from the group consisting of SEQ ID NO:31, SEQ ID NO:35, SEQ ID NO:39 and SEQ ID NO:43.

29. The probe mix of claim 23, wherein:

the target sequence of said probe is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:17 and SEQ ID NO:18; and

said one or more helper oligonucleotides include first and second helper oligonucleotides, wherein the target sequence of said first helper oligonucleotide is selected from the group consisting of SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37 and SEQ ID NO:41, and wherein the target sequence of said second helper oligonucleotide is selected from the group consisting of SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40 and SEQ ID NO:44.

30. The probe mix of claim 23, wherein:

the target sequence of said probe is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:17 and SEQ ID NO:18; and

said one or more helper oligonucleotides include first and second helper oligonucleotides, wherein the target sequence of said first helper oligonucleotide is selected from the group consisting of SEQ ID NO:30, SEQ ID NO:34, SEQ ID NO:38 and SEQ ID NO:42, and wherein the target sequence of said second helper oligonucleotide is selected from the group consisting of SEQ ID NO:31, SEQ ID NO:35, SEQ ID NO:39 and SEQ ID NO:43.

31. The probe mix of claim 23, wherein:

the target sequence of said probe is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:17 and SEQ ID NO:18; and

said one or more helper oligonucleotides include first and second helper oligonucleotides, wherein the target sequence of said first helper oligonucleotide is selected from the group consisting of SEQ ID NO:30, SEQ ID NO:34, SEQ ID NO:38 and SEQ ID NO:42, and wherein the target sequence of said second helper oligonucleotide is selected from the group consisting of SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40 and SEQ ID NO:44.

32. The probe mix of claim 23, wherein:

the target sequence of said probe is selected from the group consisting of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 and SEQ ID NO:19; and

the target sequence of one of said helper oligonucleotides is selected from the group consisting of SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37 and SEQ ID NO:41.

33. The probe mix of claim 23, wherein:

the target sequence of said probe is selected from the group consisting of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 and SEQ ID NO:19; and

the target sequence of one of said helper oligonucleotides is selected from the group consisting of SEQ ID NO:30, SEQ ID NO:34, SEQ ID NO:38 and SEQ ID NO:42.

34. An oligonucleotide for use in determining the presence of a

*Cryptosporidium parvum* organism in a test sample, said oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence contained in nucleic acid derived from a *Cryptosporidium parvum* organism, wherein the target sequence is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19 and SEQ ID NO:20

and wherein said oligonucleotide optionally includes a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

35. An oligonucleotide for use in determining the presence of a *Cryptosporidium parvum* organism in a test sample, wherein the base sequence of said oligonucleotide is at least 80% complementary to the base sequence of a target sequence contained in nucleic acid derived from a *Cryptosporidium parvum* organism, wherein the target sequence is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19 and SEQ ID NO:20, and wherein said oligonucleotide optionally includes a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

36. An oligonucleotide for use in determining the presence of a *Cryptosporidium parvum* organism in a test sample, wherein the base sequence of said oligonucleotide is fully complementary to the base sequence of a target sequence contained in nucleic acid derived from a *Cryptosporidium parvum* organism, wherein the target sequence is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19 and SEQ ID NO:20, and wherein said oligonucleotide optionally includes a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

37. A method for determining the presence of a *Cryptosporidium parvum* organism in a test sample, said method comprising the steps of:

contacting the test sample with said probe of claim 1 under stringent conditions; and

determining whether a probe:target hybrid has formed under the stringent conditions as an indication of the presence of a *Cryptosporidium parvum* organism in the test sample.

5                   38.     The method of claim 37 further comprising providing to the test sample one or more amplification primers under amplification conditions, each said primer comprising an oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence, wherein the target sequence is selected from the group consisting of SEQ ID NO:45, SEQ ID  
10     NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67 and SEQ ID NO:68, and wherein said primer optionally includes a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

15                   39.     The method of claim 38, wherein the target sequence of one of said primers is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63.

20                   40.     The method of claim 38, wherein the target sequence of one of said primers is selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64.

25                   41.     The method of claim 38, wherein the target sequence of one of said primers is selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and SEQ ID NO:65.

42. The method of claim 38, wherein the target sequence of one of said primers is selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66.

5 43. The method of claim 38, wherein the target sequence of one of said primers is selected from the group consisting of SEQ ID NO:49, SEQ ID NO:55, SEQ ID NO:61 and SEQ ID NO:67.

10 44. The method of claim 38, wherein the target sequence of one of said primers is selected from the group consisting of SEQ ID NO:50, SEQ ID NO:56, SEQ ID NO:62 and SEQ ID NO:68.

15 45. The method of claim 38, wherein said one or more primers include first and second primers, wherein the target sequence of said first primer is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63, and wherein the target sequence of said second primer is selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and SEQ ID NO:65.

20 46. The method of claim 38, wherein said one or more primers include first and second primers, wherein the target sequence of said first primer is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63, and wherein the target sequence of said second primer is selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66.

25 47. The method of claim 38, wherein said one or more primers include first and second primers, wherein the target sequence of said first primer is selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64, and wherein the target sequence of said second primer is selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and SEQ ID NO:65.

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48. The method of claim 38, wherein said one or more primers include first and second primers, wherein the target sequence of said first primer is selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64, and wherein the target sequence of said second primer is selected from the group consisting of  
5 SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66.

49. The method of claim 38, wherein said one or more primers include first and second primers, wherein the target sequence of said first primer is selected from the group consisting of SEQ ID NO:49, SEQ ID NO:55, SEQ ID NO:61 and SEQ ID NO:67, and  
10 wherein the target sequence of said second primer is selected from the group consisting of SEQ ID NO:50, SEQ ID NO:56, SEQ ID NO:62 and SEQ ID NO:68.

50. A method for determining the presence of a *Cryptosporidium parvum* organism in a test sample, said method comprising the steps of:

15 contacting the test sample with said probe of claim 20 under stringent conditions; and

determining whether a probe:target hybrid has formed under the stringent conditions as an indication of the presence of a *Cryptosporidium parvum* organism in the test sample.

51. A method for determining the presence of a *Cryptosporidium parvum* organism in a test sample, said method comprising the steps of:

contacting the test sample with said probe of claim 21 under stringent conditions; and

25 determining whether a probe:target hybrid has formed under the stringent conditions as an indication of the presence of a *Cryptosporidium parvum* organism in the test sample.

52. A method for determining the presence of a *Cryptosporidium parvum* organism in a test sample, said method comprising the steps of:

contacting the test sample with said probe of claim 22 under stringent conditions; and

determining whether a probe:target hybrid has formed under the stringent conditions as an indication of the presence of a *Cryptosporidium parvum* organism in the test sample.

53. A kit comprising, in packaged combination, said oligonucleotide of claim 34 and one or more oligonucleotides having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67 and SEQ ID NO:68, wherein said primer optionally includes a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

54. The kit of claim 53, wherein said kit includes:

a first oligonucleotide, wherein the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:18 and SEQ ID NO:19; and

a second oligonucleotide, wherein the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66 and SEQ ID NO:67.

55. The kit of claim 54, wherein:

the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17; and

5 the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63.

56. The kit of claim 54, wherein:

the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17; and

10 the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64.

57. The kit of claim 54, wherein:

15 the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17; and

the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and SEQ ID NO:65.

58. The kit of claim 54, wherein:

20 the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17; and

the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66.

25 59. The kit of claim 54, wherein:

the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18; and

the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63.

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60. The kit of claim 54, wherein:

the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18; and

5 the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64.

61. The kit of claim 54, wherein:

the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18; and

10 the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and SEQ ID NO:65.

62. The kit of claim 54, wherein:

15 the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18; and

the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66.

63. The kit of claim 54, wherein:

20 the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 and SEQ ID NO:19; and

the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63.

25 64. The kit of claim 54, wherein:

the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 and SEQ ID NO:19; and

the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64.

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65. The kit of claim 54, wherein:

the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 and SEQ ID NO:19; and

the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and SEQ ID NO:65.

66. The kit of claim 54, wherein:

the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 and SEQ ID NO:19; and

the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66.

67. The kit of claim 53, said kit including:

a first oligonucleotide, wherein the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:18 and SEQ ID NO:19;

a second oligonucleotide, wherein the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:63 and SEQ ID NO:64; and

a third oligonucleotide, wherein the target sequence of said third oligonucleotide is selected from the group consisting of SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:65 and SEQ ID NO:66.

68. The kit of claim 67, wherein:

the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17;

the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63; and

the target sequence of said third oligonucleotide is selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and SEQ ID NO:65.

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69. The kit of claim 67, wherein:

the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17;

10 the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63; and

the target sequence of said third oligonucleotide is selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66.

70. The kit of claim 67, wherein:

15 the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17;

the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64; and

20 the target sequence of said third oligonucleotide is selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and SEQ ID NO:65.

71. The kit of claim 67, wherein:

the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17;

25 the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64; and

the target sequence of said third oligonucleotide is selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66.

30

72. The kit of claim 67, wherein:

the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18;

5 the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63; and

the target sequence of said third oligonucleotide is selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and SEQ ID NO:65.

73. The kit of claim 67, wherein:

10 the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18;

the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63; and

15 the target sequence of said third oligonucleotide is selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66.

74. The kit of claim 67, wherein:

the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18;

20 the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64; and

the target sequence of said third oligonucleotide is selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and SEQ ID NO:65.

25 75. The kit of claim 67, wherein:

the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18;

the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64; and

30

the target sequence of said third oligonucleotide is selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66.

76. The kit of claim 67, wherein:

5 the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 and SEQ ID NO:19;

the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63; and

10 the target sequence of said third oligonucleotide is selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and SEQ ID NO:65.

77. The kit of claim 67, wherein:

the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 and SEQ ID NO:19;

15 the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63; and

the target sequence of said third oligonucleotide is selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66.

20 78. The kit of claim 67, wherein:

the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 and SEQ ID NO:19;

the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64; and

25 the target sequence of said third oligonucleotide is selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and SEQ ID NO:65.

79. The kit of claim 67, wherein:

30 the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 and SEQ ID NO:19;

the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64; and

the target sequence of said third oligonucleotide is selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66.

5

80. The kit of claim 53, wherein said kit includes:

a first oligonucleotide, wherein the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:8, SEQ ID NO:12, SEQ ID NO:16 and SEQ ID NO:20; and

10

a second oligonucleotide, wherein the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:67 and SEQ ID NO:68.

15

81. The kit of claim 80, wherein the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:49, SEQ ID NO:55, SEQ ID NO:61 and SEQ ID NO:67.

20

82. The kit of claim 80, wherein the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:50, SEQ ID NO:56, SEQ ID NO:62 and SEQ ID NO:68.

25

83. The kit of claim 53, wherein said kit includes:

a first oligonucleotide, wherein the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:8, SEQ ID NO:12, SEQ ID NO:16 and SEQ ID NO:20;

30

a second oligonucleotide, wherein the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:49, SEQ ID NO:55, SEQ ID NO:61 and SEQ ID NO:67; and

a third oligonucleotide, wherein the target sequence of said third oligonucleotide is selected from the group consisting of SEQ ID NO:50, SEQ ID NO:56, SEQ ID NO:62 and SEQ ID NO:68.

5                   84.     A kit comprising, in packaged combination, said probe of claim 1 and  
at least one helper oligonucleotide having an at least 10 contiguous base region which is at  
least 80% complementary to an at least 10 contiguous base region present in a target sequence  
selected from the group consisting of SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ  
ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37,  
10   SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID  
NO:43 and SEQ ID NO:44.

                  85.     A kit comprising, in packaged combination, said probe of claim 1 and  
an amplification primer comprising an oligonucleotide having an at least 10 contiguous base  
15   region which is at least 80% complementary to an at least 10 contiguous base region present  
in a target sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:46,  
SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID  
NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57,  
SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID  
20   NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67 and SEQ ID NO:68,  
wherein said primer optionally includes a 5' sequence which is recognized by an RNA  
polymerase or which enhances initiation or elongation by an RNA polymerase.

                  86.     The kit of claim 85 further comprising at least one helper  
25   oligonucleotide having an at least 10 contiguous base region which is at least 80%  
complementary to an at least 10 contiguous base region present in a target sequence selected  
from the group consisting of SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID  
NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37,  
SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID  
30   NO:43 and SEQ ID NO:44.